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Conference Abstract

Mainstreaming Molecular Biodiversity: A call for a unified and interoperable framework

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Abstract

Over the past 20 years, immense progress has been made in enhancing the effectiveness, affordability, and deployability of molecular methods for biodiversity assessment and monitoring. From the micro- to macroscopic scale, methods such as amplicon sequencing of phylogenetic marker genes, metagenomics, and metatranscriptomics have greatly impacted biology and ecology, and are steadily being integrated into national and international biodiversity policy. Over the next decade, technologies such as miniaturised and autonomous DNA sequencing platforms will amplify this momentum, ushering in an unprecedented volume of deeply minable biodiversity information. While production-grade resources exist to standardise, archive, and exchange raw molecular data (e.g. the resources of the International Nucleotide Sequence Database Collaboration (INSDC) for DNA and RNA sequences), there are still no equivalent frameworks for biodiversity information derived from molecular methods. Research infrastructures in both the biodiversity and molecular biology domains must fill this gap with great urgency to channel molecular advances into efforts to understand and sustain Earth's imperilled biosphere.

This session seeks to accelerate the implementation of global standards to link molecular biodiversity data to taxonomy-based systems. Only with these in place can we realise a robust, distributed, yet fully interoperating, network of infrastructures, projects, and researchers addressing molecular biodiversity. This introductory series of flash talks will

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present the rationale and goals of the session, alongside a joint vision from representatives of several convening stakeholders. A contribution from ELIXIR, an intergovernmental organisation of distributed infrastructures for biological data, will demonstrate the high readiness of biological data resources such as the European Nucleotide Archive (ENA) to mobilise molecular data along new standards. An intervention from the SILVA rRNA database project - itself an ELIXIR Core Data Resource - will note the actionability of interfacing molecular-based phylogenies with Linnaean systems hosted by partners such as the Global Biodiversity Information Facility (GBIF). Two more contributions will emphasise the essential role (and thus critical need) of molecular biodiversity standards in bridging research and operations. The first will focus on the nation-scale Metagenomics-Based Ecosystem Biomonitoring (EcoBiomics) project in Canada, which is using 'omic approaches to better assess, monitor, and remediate microbial and invertebrate biodiversity in soil and aquatic ecosystems, thus sustaining ecosystem resilience and service provision upon which society and economies depend. The second will underscore the need for international and stable standards to advance the long-term mission of the Global Omics Observatory Network (GLOMICON), and its contribution to the Global Ocean Observing System's Essential Ocean Variables (GOOS EOVs) under the Intergovernmental Oceanographic Commission of the United Nations Educational, Scientific, and Cultural Organization (IOC-UNESCO). Collectively, these contributions will make the case for a concerted effort to expedite the principled creation of operational information standards in molecular biodiversity. We invite all stakeholders to join us in implementing these standards in the coming years.

Keywords

omics, genomics, taxonomic marker genes, infrastructure, molecular, microbes, eDNA, biodiviersity, infrastructure

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Conflicts of interest

None